

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 17:40:54 ; Search time 43 Seconds  
(without alignments)  
1798.882 Million cell updates/sec

Title: US-09-635-501-2  
Perfect score: 4291  
Sequence: 1 MSSSSWLLSLVAVTAQAQT.....ISKGNPQFNTDDVQTSF 805

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4281	99.8	804	2 T14762	hypothetical prote
2	1344	31.3	732	1 S05238	peptidyl-di-peptida
3	1337	31.2	1306	1 A31759	peptidyl-di-peptida
4	1334	31.1	732	1 A35655	peptidyl-di-peptida
5	1334	31.1	1312	1 A34171	peptidyl-di-peptida
6	1312	30.6	1193	2 JC2489	peptidyl-di-peptida
7	1310	30.5	1313	1 JC2038	peptidyl-di-peptida
8	1283	29.9	737	1 A34402	peptidyl-di-peptida
9	1283	29.9	1309	1 S35484	peptidyl-di-peptida
10	1058	24.7	611	2 S65472	peptidyl-di-peptida
11	1039	24.2	615	2 A57533	peptidyl-di-peptida
12	1030	24.0	630	2 JC5374	peptidyl-di-peptida
13	642.5	15.0	907	2 T15792	angiotensin-conver
14	157	3.7	532	2 C83696	hypothetical prote
15	154	3.6	502	2 AF1310	hypothetical prote
16	147	3.4	502	2 AE1682	probable thermosta
17	139.5	3.3	987	2 AI2011	probable synthetase
18	139	3.2	608	2 B82938	zinc metalloprotei
19	136	3.2	611	2 D28861	zinc metalloprotei
20	135	3.1	501	2 D69943	carboxypeptidase h
21	125	2.9	627	1 A40048	1,4-alpha-glucan b
22	124.5	2.9	987	2 I48373	G-utrophin - mouse
23	124	2.9	538	2 E72561	probable thermosta
24	123.5	2.9	902	2 E90270	conserved hypotet
25	123	2.9	990	2 S23416	antibiotic epider
26	122	2.8	642	2 E98000	1,4-alpha-glucan b
27	121	2.8	607	2 AB3511	oligoendopeptidase
28	121	2.8	1034	2 T30574	beta-galactosidase
29	120	2.8	1339	2 A84683	probable SNF2 subf

ALIGNMENTS

RESULT 1

T14762  
hypothetical protein DKFZp434A014.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C:Accession: T14762  
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999  
A:Reference number: Z18181  
A:Accession: T14762  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-804 <WAM>  
A:Cross-references: EMBL:AL110224  
A:Experimental source: adult testis; clone DKFZp434A014  
C:Genetics:  
A:Note: DKFZp434A014.1

Query Match 99.8%; Score 4281; DB 2; Length 804;  
Best Local Similarity 99.9%; Pred. No. 6.7e-286;  
Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	SSSSWLLSLVAVTAQAQTIEEQAKTFLDKFNHRAEDLFYQSSLASWNYNTNITENVNQ	61
DB	1	SSSSWLLSLVAVTAQAQTIEEQAKTFLDKFNHRAEDLFYQSSLASWNYNTNITENVNQ	60
QY	62	MNAGDKWSAFLEKQSTLAQMPLOEIONLVKLOLQALQNGSSVLSEDKSKRLNTILN	121
DB	61	MNAGDKWSAFLEKQSTLAQMPLOEIONLVKLOLQALQNGSSVLSEDKSKRLNTILN	120
QY	122	TMSTIYSTGKVCNPDNPOECILLPEGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE	181
DB	121	TMSTIYSTGKVCNPDNPOECILLPEGLNEIMANSLDYNERLWAWESRSEVGKQLRPLYE	180
QY	182	EYVVLKNEMARANHYEDGYWRGDYEVNGVDYDYSRGQLTIEDVEHTFEETKPLYEHLH	241
DB	181	EYVVLKNEMARANHYEDGYWRGDYEVNGVDYDYSRGQLTIEDVEHTFEETKPLYEHLH	240
QY	242	AYVRAKLMAVPSYISPGCLPAHLIGDMGFRFTNLSLTVFGQKNIDVTDAMVQQA	301
DB	241	AYVRAKLMAVPSYISPGCLPAHLIGDMGFRFTNLSLTVFGQKNIDVTDAMVQQA	300
QY	302	WDAQRIKFAEKFFVSVGLPNNMTQGFWNSMLTDPGNQKAVCHPTANDLKGDFRILMC	361
DB	301	WDAQRIKFAEKFFVSVGLPNNMTQGFWNSMLTDPGNQKAVCHPTANDLKGDFRILMC	360
QY	362	TKVTMDDFLTAHMGHTQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKSI	421
DB	361	TKVTMDDFLTAHMGHTQYDMAYAAQPFLLRNGANEGFHEAVGIMSLSAATPKHLKSI	420
QY	422	GLLSPOFQEQNETEINFLLKQALATVGLPTVYMLEKRWVWVFKGEIPEKDDQMKRWENK	481

SWI1 protein homol  
TRAP-like protein  
cytoplasmic dynein  
hypothetical prote  
1,4-alpha-glucan b  
conserved hypotet  
NMDA receptor-bind  
probable S-layer p  
probable oligoendo  
utrophin - human  
thermostable carbo  
hypothetical prote  
hypothetical colle  
phage infection pr  
hypothetical prote

```
Db 421 GLLSPDFQEDNETEIFLKLQALTIQVTLPTTYMLEKRWVFKGEIPKQDQWKKWEMK 480
QY 482 RELVGVVEVPVHDETYCDPASLFHVSNDYSFIRYTRTYLQYQFOFQALCOAAKHGPHLK 541
Db 481 RELVGVVEVPVHDETYCDPASLFHVSNDYSFIRYTRTYLQYQFOFQALCOAAKHGPHLK 540
QY 542 CDSNSTAGOKLFNMLRLGKSEPTWTLALENVVGVAKNMVRLNLYFFLEFWLKDQKN 601
Db 541 CDSNSTAGOKLFNMLRLGKSEPTWTLALENVVGVAKNMVRLNLYFFLEFWLKDQKN 600
QY 602 SFVGVSTWSPYADQSIKVRISLKSGALGDYKAYEMNDNEMYLPRSSVAYAMROYFLKVKQ 661
Db 601 SFVGVSTWSPYADQSIKVRISLKSGALGDYKAYEMNDNEMYLPRSSVAYAMROYFLKVKQ 660
QY 662 MILFGEEDVRVANLKRISFNFTVAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDS 721
Db 661 MILFGEEDVRVANLKRISFNFTVAPKNVSDIIPRTEVEKAIKMSRSRINDAFRLNDS 720
QY 722 LEFLGIQTLGPPNPPVSIWLVFVGVVGVIVGVILIFTGIRDRKKKKARSGENPY 781
Db 721 LEFLGIQTLGPPNPPVSIWLVFVGVVGVIVGVILIFTGIRDRKKKKARSGENPY 780
QY 782 ASIDISKGENNFGQNTDDVQTSF 805
Db 781 ASIDISKGENNFGQNTDDVQTSF 804

RESULT 2
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, testicular splice form - human
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypeptidase
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999
C:Accession: S05238; A33979
R:Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F.
FEBS Lett. 252, 99-104, 1989
A:Title: The testicular transcript of the angiotensin I-converting enzyme encodes for the
A:Reference number: S05238; MUID:89338720
A:Accession: S05238
A:Molecule type: mRNA
A:Residues: 1-732 <LAT>
A:Cross-references: EMBL:X16295; NID:g28264; PIDN:CAA34362.1; PID:g28265
R:Ehlers, M.R.W.; Fox, E.A.; Stydman, D.J.; Riordan, J.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989
A:Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis
A:Reference number: A33979; MUID:90046671
A:Accession: A33979
A:Molecule type: mRNA
A:Residues: 1-732 <EHL>
A:Cross-references: GB:M26657; NID:g338666; PIDN:AAA60611.1; PID:g338667
A:Experimental source: clones R1.2 and T8B
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
C:Comment: For the renal and pulmonary splice form, see PIR:A31759.
C:Genetics:
A:Gene: GDB:DCPI; ACE
A:Cross-references: GDB:119840; OMIM:106180
A:Map position: 17q23-17q23
C:Function:
A:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptide
C:Superfamily: mammalian peptidyl-di-peptidase A
C:Keywords: alternative splicing; glycoprotein; metalloproteinase; peptidyl dipeptide hyd
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-732/Product: peptidyl dipeptidase I #status predicted <MAT>
F:686-702/Domain: transmembrane #status predicted <TRM>
F:103,121,140,186,368,617/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:414,418,434/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F:415/Active site: Glu #status predicted

Query Match 31.3%; Score 1344; DB 1; Length 732;
Best Local Similarity 41.8%; Pred No. 7 6e-85;
Matches 259; Conservative 119; Mismatches 204; Indels 38; Gaps 10;

QY 15 TAAQS-----TIEQAKTFIDKFNHEADLFYQSSLASWYNTNITTEE-----NVQNM 62
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Db 61 TSAQSPNLVDEAEASKFVEEYDRTSQVVMVEAEANWNTNITTSKILLQKNMQIA 120
QY 63 NNAGDKWSAFLEQSTLAQMYPLQELQNTVTKLQALQOQSSVLSDEKSKRLNTILMT 122
Db 121 NIT-----LKYQTAARKFDVQNLQNTIKRIKKVQDQLERAAALPAQELEENKILLD 172
QY 123 MFTIYSTGVKQPNPQECLELLPEGLNETMANSLDYNERLWAWESWRSVQKQLRPLYEE 182
Db 173 MFTIYSTGVKQPNPQECLELLPEGLNETMANSLDYNERLWAWESWRSVQKQLRPLYEE 182
QY 183 YVYLKEMARAHYEDYDWRGDYEVNGVDGYDYSRGOLIEDVEHTPEEIKPLYEHLHA 242
Db 231 YVELLNOAARNGYVDAGDSWRSMTETPSLE-----QDLERLFOELQPLYLNLHA 280
QY 243 YVRAKLMNAY-PSYISPIGCLPAHLGLDMGREFWTLNLSLTPFGOKPNIDVTDAVDOA 301
Db 281 YVRAKLMNAY-PSYISPIGCLPAHLGLDMGREFWTLNLSLTPFGOKPNIDVTDAVDOA 301
QY 302 WDAQRIFFAEKFFSVSVGLPNMTQGFWENSLTDPGNVOKAVCHPTAWDLGKG-DFRILM 360
Db 341 WTPRRMEKADDFETSLGLLPVPEFWNKSMLEKPTDGVVVCASAWDFYNGKDFRIKQ 400
QY 361 CTKVYMDDFLTAHHMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSATPKHLKS 420
Db 401 CTTVNLDELVAHHMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSATPKHLKS 420
QY 421 IGLLSPDFQEDNETEIFLKLQALTIQVTLPTTYMLEKRWVFKGEIPKQDQWKKWEM 480
Db 461 LNLSSSEGSD-EHDINFLMKALDKIAPFYSYLVQDWRVDFGSIKENTYNQEWWSL 519
QY 481 KREIVGVVEVPVHDETYCDPASLFHVSNDYSFIRYTRTYLQYQFOFQALCOAAKHGPHLK 540
Db 520 RLKYQGLCPVPVHDETYCDPASLFHVSNDYSFIRYTRTYLQYQFOFQALCOAAKHGPHLK 540
QY 541 KCDISNSTAGOKLFNMLRLGKSEPTWTLALENVVGVAKNMVRLNLYFFLEFWLKDQKN 600
Db 580 KCDIYQSKAGORLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFRLDLWLTENE 639
QY 601 --NSFVGW-STOWSPYADQS 617
Db 640 LHGEKLGWPOYNNWTPNSARS 659
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RESULT 3
A31759
peptidyl-di-peptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - hum
N:Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxype
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999
C:Accession: A31759; PQ0004
R:Soubrier, F.; Alhenc-Gelas, P.; Hubert, C.; Allegrini, J.; John, M.; Tregear, G.; C
Proc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988
A:Title: Two putative active centers in human angiotensin I-converting enzyme reveal
A:Reference number: A31759; MUID:89071703
A:Accession: A31759
A:Molecule type: mRNA
A:Residues: 1-1306 <SOU>
A:Cross-references: GB:J04144; NID:g178285; PIDN:AAA51684.1; PID:g178286
A:Experimental source: kidney
A:Note: parts of this sequence, including the amino end of the mature protein, were d
R:Takeuchi, K.; Shimizu, T.; Ohishi, N.; Seyama, Y.; Takaku, F.; Yotsumoto, H.
J. Biochem. 106, 442-445, 1989
A:Title: Purification of human lung angiotensin-converting enzyme by high-performance
A:Reference number: PQ0004; MUID:90110025
A:Accession: PQ0004
A:Molecule type: protein
A:Residues: 'XX',32-34,'E',36-37,'X',39-41,'R',43-46 <TAK>
A:Experimental source: lung
C:Comment: This splice form is found in many tissues, in particular kidney and lung v
C:Genetics:
A:Gene: GDB:DCPI; ACE
A:Cross-references: GDB:119840; OMIM:106180
```

A:Map position: 17q23-17q23  
A:Function:  
A:Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptides  
A:Note: plays a role in the control of blood pressure by catalyzing the conversion of an angiotensinogen to angiotensin  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; me  
F:1-29/Domain: signal sequence; status predicted <SIG>  
F:30-1306/Product: peptidyl dipeptidase I #status predicted <MAT>  
F:1260-1276/Domain: transmembrane #status predicted <TRM>  
F:36,54,74,111,146,160,318,445,509,523,677,695,714,760,942,1191,1225/Binding site: carb  
F:390,394/Binding site: zinc #status predicted  
F:988,992,1008/Binding site: zinc, catalytic (His, His, Glu) #status predicted  
F:989/Active site: Glu #status predicted

Query Match 31.2%; Score 1337; DB 1; Length 1306;  
Best Local Similarity 41.7%; Pred. No. 5.6e-84;  
Matches 255; Conservative 118; Mismatches 204; Indels 34; Gaps 9;

QY 20 TIEQAKFLDKFNHEAEDLFYQSSLASNNYNTNITEE-----NVQNMNAGDKWSA 71  
DB 644 TDEAASKFVEEYDTSQVWNEYAEANNYNTNITETSKILLQKNQJANH----- 697

QY 72 FLKEOSTLAQMTPLQIOLNLTVKLQALQNGSSVLSDESKSKRLNTILNTMTSTIYSTGK 131  
DB 698 --LKYGTQARKPDVNOLONTTKRIKKVQDLEAALPAQLEENKILLDMETTSYAT 755

QY 132 VCNPDNPOBCLLEPLGELMEIANSLDYNERLWAWESRSEVKGQRLRPLYEYVVLKNEMA 191  
DB 756 VCHPVG--SCIQLEPDNLNVAATSKRYEDLLWAGWRDKAGRAILOFPYKVELINQAA 813

QY 192 RANHYEDYGVYRGDYEYNGVDYDYSRGQIEDVEHTFEELKPLYEHLHAYVRRAKLMA 251  
DB 814 RLVGVVDAGDSWRSYETPSLE-----QDLERFLQELQPLYLNLHAYVRRAHLRH 863

QY 252 Y-PSYISPLGCLPAHLGDMGRFTNLISLVTFPGQKPNIDYTDAMVDQAWDAQRIKPE 310  
DB 864 YGAQHINLEGPFAHLGDMMAQTSNIYDLVVPFSPASMDTTEAMLKQGTTPRRMFEK 923

QY 311 AEKFFVSVGLPNNTOGFWNSMLTDPGNVQKAVCHPTAWDLGK--DFRILMCTKVTWDDFLTAHHEMG 377  
DB 924 ADDEFTSLGLLPVPEFNWKSMLERPTDGVREVCHASAWDFYNGDKDFKQCTVTYNLEDL 983

QY 370 LTAHEMHQIYQDMAYAAQPFLLRNGANEGFHEAVGEMTSLAAATPKHUKSLGLSPDPQ 429  
DB 984 VVAHHEMHQIYFMQYKDLPAVALREGANPGFHEATGDLVALSVSTPKHLHSLNLSSEGG 1043

QY 430 EDNETELNPLKQALTYGTLPFTYMLEKRWKMWKFGKPTKQDWKMKWEMRETVGVVE 489  
DB 1044 SD-EDHINFLMKALDKIAFIPFSLVQNRWRVFDGSIKENYQEWMSLRKLYQGGLCP 1102

QY 490 PVPHDETYCDPASLPHVSNDSYFIRYTRTYLQFOFQALCOAAKHEGPHKCDISNSTE 549  
DB 1103 PVPRQGDGDPGAKFHPSPVPIRYFVSFIQFQFHEALCOAAGHTGPLHKCDIYQSK 1162

QY 550 AQOKLENMLRCKSPWTLALENVVCAKMMNVRPLNLTPEPLFTWLKQDNK--NSFVGV- 506  
DB 1163 AGORLATAKLGFSRPPWPAQMLITGQPNMNSASAMLSYFKPLDLLRLTENELHGEKLGWP 1222

QY 607 STDWSPYADQS 617  
DB 1223 QYNWTPNSARS 1233

RESULT 4  
A35655  
peptidyl-dipeptidase A (EC 3.4.15.1), testis - mouse  
N:Alternate names: peptidyl-dipeptidase I, testis  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A35655  
R:Howard, T.E.; Shai, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E.  
Mol. Cell. Biol. 10, 4294-4302, 1990  
A:Title: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated w

A:Reference number: A35655; MUID:90318396

A:Accession: A35655

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-732 <HOW>

C:Cross-references: GB:M55333; NID:q191589; PIDN:AAA37149.1; PID:q191590

C:Superfamily: mammalian peptidyl-dipeptidase A

C:Keywords: alternative splicing; peptidyl dipeptide hydrolase; transmembrane protein

Query Match 31.1%; Score 1334; DB 1; Length 732;

Best Local Similarity 42.6%; Pred. No. 3.7e-84;

Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

A:Accession: A29220  
A:Molecule type: mRNA  
A:Residues: 1-332 <BE2>  
A:Cross-references: GB:J03940; NID:g191583; PIDN:AAA37146.1; PID:g191584  
R:Bernstein, K.E.; Martin, B.M.; Striker, L.; Striker, G.  
Kidney Int. 33, 652-655, 1988  
A:Title: Partial protein sequence of mouse and bovine kidney angiotensin converting enzyme  
A:Reference number: A61477; MUID:86215372  
A:Accession: A61477  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 35-54 <BE3>  
A:Experimental source: kidney  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; blood pressure control; membrane protein; peptidyl-dipeptidase A  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-1312/Product: peptidyl dipeptidase I #status predicted <AT>

Query Match 31.1%; Score 1334; DB 1; Length 1312;  
Best Local Similarity 42.6%; Pred. No. 9.2e-84;  
Matches 255; Conservative 112; Mismatches 213; Indels 18; Gaps 7;

QY 20 TTEQAKFLDKFNHEADLFYQSSLASWNTNITENVNQNNAGDKWSAFLKEOSTL 79  
DB 649 TDEAKADRFVEYDRTAQVLLNEAYEANNQYNTNITIEGSKILLEKSTEVSNHTLUYGR 708  
QY 80 AQMYPLQEIQLTVKQLQALQONGSSVLSEDSKSRKRLNTILNTMTSTYTGKVCNPDNPQ 139  
DB 709 AKTEDVSNFQSSIKRIIKLQNLQRAVLPPKELEENQILLDMETYSLSNICYTNG-- 766  
QY 140 ECLLLEPGLEINMANSLDYNERLWAWESRSEVQKQLRPLYEEVVLKKNEMARAHYEDY 199  
DB 767 TCMPLDPLTNMARSRYEELLMWKSRRKVRGAILPFPFFYFNFSSNKIAKNGYTD 826  
QY 200 GDYWRGDYEVNGVDGYDSRGOLIEDVEHTEEIKPLXEHHLHAYRAKLMAVPS-YISP 258  
DB 827 GDSWRLTESDNL-----QDLEKLYQELQPLYLNLHAYRRSLHRYGSEIYINL 876  
QY 259 IGCLPAHLGLDGMGRFTNLYSLTVPFQGNIDVTDAMVDQAWDAQRIKFAEKFFSV 318  
DB 877 DGPPIAHLGLNMAQWTSNIYDLVAPFSPAPNIDATEAMIKQWTPRIFKEADNFFETSL 936  
QY 319 GLPNTQGFWNSMLTDPGNQKAVCHPTAWDLGK-DFRILMCTKYTMDDFLTAHHENG 377  
DB 937 GLLPFPPEFWNKSMLKPTDGVGVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHENG 996  
QY 378 HQYDMVAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437  
DB 997 HQYPMQKDLPTVREGANPGFHEAIGDMALSSTPKHLISLNLSTE-OSGYEYDIN 1055  
QY 438 FLKQALITVGLPTPTMYLEKRWNVFKEIPKQDMKKWEMKREIVGVVPEVPHDET 497  
DB 1056 FLMKALDKIAIPFSSYLIDQWRWRVFDGSIKENYNQEWSLRLKYQGLCPVPRSQD 1115  
QY 498 CDPSLIFHVSNDYFIRYTRTYQFQEQALCQAKHGGPLHKCDISNSTEAGOKLFN 557  
DB 1116 FDPGSKFHPANVPYIRYFVSVIOFQFHALCRAAGTGPHLKDIIYQSKKAGKLADA 1175  
QY 558 LRLGKSEPTWTLALENVVGAKNNVRPLNLYFEPLFTWLDQNK--NSFVGW-STDWSP 612  
DB 1176 MKLGYSKWPPEAMKLTIGQPNNSASAMNYPKPLTEWLVTENRRHGETLGVPEYNWAP 1233

RESULT 6  
JC2489  
N:Alternate names: angiotensin converting enzyme  
C:Species: Gallus gallus (Chicken)  
C:Date: 16-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 28-May-1999  
C:Accession: JC2489  
R:Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.  
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994  
A:Title: Chicken lacks the testis specific isozyme of angiotensin converting enzyme found

A:Reference number: JC2489; MUID:95110342  
A:Accession: JC2489  
A:Molecule type: mRNA  
A:Residues: 1-1193 <EST>  
A:Cross-references: NID:g685168; PIDN:AAA75554.1; PID:g994708  
C:Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase that cleaves a  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc  
F:316,331,914,929/Binding site: zinc, catalytic (Glu, His, Glu, His) #status predicted

Query Match 30.6%; Score 1312; DB 2; Length 1193;  
Best Local Similarity 40.4%; Pred. No. 2.6e-82;  
Matches 264; Conservative 110; Mismatches 243; Indels 36; Gaps 10;

QY 22 EQQAKTFLDKFNHEADLFYQSSLASWNTNITENVNQNNAGDKWSAFLKEOSTLAQ 81  
DB 544 EQQAKTFLDKFNHEADLFYQSSLASWNTNITENVNQNNAGDKWSAFLKEOSTLAQ 81  
QY 82 MYPLQEIQLTVKQLQALQONGSSVLSEDSKSRKRLNTILNTMTSTYTGKVCNPDNP--P 138  
DB 604 QFDPSPQEDTETVRIILKLSVLRALPDELKEYNATLLSDMETTYSVAKVRENNTFHP 663  
QY 139 QECLLLEPGLEINMANSLDYNERLWAWESRSEVQKQLRPLYEEVVLKKNEMARAHYED 198  
DB 664 -----LDPLDLDILATSRDYNELLFQWQWASGAKIKDKYKRYVELSKAAVLNGYTD 718  
QY 199 YGDYWRGDYEVNGVDGYDSRGOLIEDVEHTEEIKPLXEHHLHAYRAKLMAVPS-PSYIS 257  
DB 719 NGAYWRLSYETTFE-----EDLERLYQLQPLYLNLHAYRRSLHRYGSEIYINL 768  
QY 258 PGCLPAHLGLDGMGRFTNLYSLTVPFQGNIDVTDAMVDQAWDAQRIKFAEKFFSV 317  
DB 769 LKGPPIAHLGLNMAQWTSNIYDLVAPFDPDATKVDATPAKQCGWTPKMMFEESDRFFTS 828  
QY 318 VGLPNTQGFWNSMLTDPGNQKAVCHPTAWDL-GKGFRLMCTKYTMDDFLTAHHEM 376  
DB 829 LGLIPMPQEFWQKSMLEKPADGVGVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEM 888  
QY 377 GHQYDMVAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETE 436  
DB 889 GHVQYFLQYMDQPIFRDGCANPGFHEAIGDMALSSTPKHLISLNLDD-OVTENEESDI 947  
QY 437 NFLKQALITVGLPTPTMYLEKRWNVFKEIPKQDMKKWEMKREIVGVVPEVPHDET 496  
DB 948 NYLMSIALDKIAIPFSSYLIDQWRWRVFDGRIKEDSYNQWNLRLKYQGLCPVPRSD 1007  
QY 497 YCDPSLIFHVSNDYFIRYTRTYQFQEQALCQAKHGGPLHKCDISNSTEAGOKLFN 556  
DB 1008 DFDPGAKFHPANVPYIRYFVSVIOFQFHALCRAAGTGPHLKDIIYQSKKAGKLGD 1067  
QY 557 MLRLGKSEPTWTLALENVVGAKNNVRPLNLYFEPLFTWL--KDNKNSFVGW-STDWSP 613  
DB 1068 AMKLGFSKWPPEAMKLTIGQPNNSAALMSYFELPTWLVKNTENGELGVNPEYSWTPY 1127  
QY 614 ADQSIVKRLSLKSLG-----DKAYENDNEMYLFRSSSVAVAMQYFLKVK 659  
DB 1128 AVTEPHATDTADFLGNSVGTQKNTAGW-----VLLALALVELITSIFLGVK 1175

RESULT 7  
JC2038  
N:Alternate names: angiotensin converting enzyme; kininase II  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JC2038  
R:Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.  
Biochem. Biophys. Res. Commun. 198, 380-386, 1994  
A:Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs  
A:Reference number: JC2038; MUID:94121658  
A:Accession: JC2038  
A:Molecule type: mRNA  
A:Residues: 1-1313 <KOI>

A:Cross-references: GB:J05041; NID:9437289; PIDN:AAA82111.1; PID:9437290  
A:Note: The authors translated the codon ACC for residue 159 as Tyr  
C:Comment: This enzyme is a zinc-containing dicarboxy peptidase that cleaves angiotensin I  
C:Comment: This enzyme plays a critical role in blood pressure homeostasis and is the ta  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; peptidyl-dipeptide hydrolase; transmembrane protein; z  
F:393-400,990-998/Region: catalytic status predicted  
F:1264-1284/Domain: transmembrane #status predicted <TM>

Query Match 30.5%; Score 1310; DB 1; Length 1313;  
Best Local Similarity 42.0%; Pred. No. 4.2e-82;  
Matches 251; Conservative 115; Mismatches 214; Indels 18; Gaps 7;

QY 20 TIEQAKTFDKFHEAEFLFYQSSLSASWYNTNITERNVQNMNAGDKWSAFLEKEQSTL 79  
DB 650 TDEAKRFRVEEYDRTAKVLWNEYAEANWYNTNITIEGSKILLQKNEVSNHLLKYGTW 709  
QY 80 AQMPYLOEIQNLTKVLQALQOQNGSSVLSEDSKRLNTILNTSTIYSTGKVCNPDNPQ 139  
DB 710 AKTFDVSNTQSTIKRIKKVQNDRAVLPPNELEEYNOILLDMETTYSVANVCYTG-- 767  
QY 140 ECLLEPPGNEIMANSLDYNERLWAWESRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199  
DB 768 TCLSLEPDLTNIMATSRKYEELWVWKSWRDKVGRAILPPFPKYVDFSNKIAKLNGYSDA 827  
QY 200 GDYWRGDYEVNGVDGYDSRGQLIEDVEHTEFKPLYEHLYHAYVRKLMNAYPS-YISP 258  
DB 828 GDSWRSSYESDDLE-----QDLKLYQELQPLNLHAYVRRSLRHHYSEYINL 877  
QY 259 IGLPAHLGLGDMWGRFTNLYSLTVPGQKPNIDVTAMVDQANDQARIFPEAEKFFVSV 318  
DB 878 DGPFAHLGLGNWAQVNSIYDLVAPPPSAPSIDATEAMIKOGTTPRIFKEADNFTSL 937  
QY 319 GLPNMTQGWNSMLTDPGNVOKAVCHPTAWDLGKG--DFRILMCTKVTMDDFLTAHHEG 377  
DB 938 GLLPVPPEFWNKSMLKEPTDGRVNVCHASAWDFVNGDFRDKQTSVNEELVIAHHEG 997  
QY 378 HIQYDMAYAAQFLLRNGANEGHEAVGEIMSLSAATPKHLKSLGLSPDQEDNETEIN 437  
DB 998 HIQYFMQYKDLPTVTEREGANPGFHEAIGDVLALSVSPKHLHSLNLLSSE--GSGYEHDI 1056  
QY 438 FLLKQALITVGLTPFTYMLEKRWMPKGEIPKQDWMKKWEMKREIVGVPPHDETY 497  
DB 1057 FLMKALDKIAFIPFSYLLDQWRVFDGSIITKENYQEWNSLRKYQGLCPVPRSQD 1116  
QY 498 CDPASLPHVSNDSYRIVYRTRLYQFQFQALCOAAKHEGPHKCDLSNSTEAGOKLFNM 557  
DB 1117 FDPGSKFHPANVPYRIVYRISFIQFQFHEALCRAGHTGPLYKCDIYQSKAEGKLLADA 1176  
QY 558 LRLKSEPTWLALENVVGAKNMNVRLLNYPFLTWLKDQNK--NSFVGW-STDWSP 612  
DB 1177 MKLGYSKQWPEAMKITGQPNMSASAIMVFKPLTEWLVTEVNRHGETLGPWETWTP 1234

RESULT 8  
A34402  
peptidyl-dipeptidase A (BC 3.4.15.1) precursor, testicular - rabbit  
N:Alternate names: angiotensin I-converting enzyme; dipeptidyl carboxypeptidase I; pepti  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A34402; A60724; A36232; C18700  
R:Kumar, R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.  
J. Biol. Chem. 264, 16754-16758, 1989  
A:Title: Structure of testicular angiotensin-converting enzyme. A segmental mosaic isozyme  
A:Reference number: A34402; MUID:89380303  
A:Accession: A34402  
A:Molecule type: mRNA  
A:Residues: 1-737 <KUM>  
A:Cross-references: GB:J05041; NID:g164744; PIDN:AAA31153.1; PID:g164745  
R:Sen, G.C.; Thekkumkara, T.J.; Kumar, R.S.  
J. Cardiovasc. Pharmacol. 16(Suppl.4), S14-S18, 1990  
A:Title: Angiotensin-converting enzyme: structural relationship of the testicular and the  
A:Reference number: A60724; MUID:91155372

A:Accession: A60724  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 73-173 <SEN>  
A:Note: identical sequences were obtained for mRNAs from lung and testes  
R:Chen, Y.N.P.; Riordan, J.F.  
Biochemistry 29, 10493-10498, 1990  
A:Title: Identification of essential tyrosine and lysine residues in angiotensin conv  
A:Reference number: A36232; MUID:91104959  
A:Accession: A36232  
A:Molecule type: protein  
A:Residues: 154-160;236-242 <CHE>  
R:Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.  
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982  
A:Title: The NH2-and COOH-terminal sequences of the angiotensin-converting enzyme iso  
A:Reference number: A90107; MUID:83048249  
A:Accession: C18700  
A:Molecule type: protein  
A:Residues: 33-35; 'SN',38-39; 'SS','FAEL',737 <IWA>  
C:Note: several of the amino acids in reported are tentative  
C:Comment: The pulmonary and testicular isoforms of this enzyme differ substantially  
ggests that the two isoforms arise by alternative splicing of one gene.  
C:Superfamily: mammalian peptidyl-dipeptidase A  
C:Keywords: alternative splicing; peptidyl-dipeptide hydrolase; testis; transmembrane

Query Match 29.9%; Score 1283; DB 1; Length 737;  
Best Local Similarity 40.8%; Pred. No. 1.3e-80;  
Matches 250; Conservative 112; Mismatches 213; Indels 38; Gaps 10;

QY 20 TIEQAKTFDKFHEAEFLFYQSSLSASWYNTNITIEE-----NVQNMN--AGDKW 69  
DB 75 TDEAEASRFEVEYDRSFQAVNWEYAEANWYNTNITIEASKILLQKMQIANHTLVGNW 134  
QY 70 SAFLEKESTLAQMPYLOEIQNLTKVLQALQOQNGSSVLSEDSKRLNTILNTSTIYST 129  
DB 135 -----ARREDVSNFQNAISRRIKKVQDLQRAVLVPVKELEYNQILLDMETIYSV 184  
QY 130 GKYCNPNPQSCLLLEPGNEIMANSLDYNERLWAWESRSEVGKQLRPLYEEYVVLKNE 189  
DB 185 ANVCRVDG--SCLEPDLTNLMATSRKYDELLWVTSWRDKVGRAILPPFPKYVEETNK 242  
QY 190 MARANHYEDYGDYWRGDYEVNGVDGYDSRGQLIEDVEHTEFKPLYEHLYHAYVRKLM 249  
DB 243 AARLNGYVDAGDSRSMYETPLE-----QDLERLFQELQPLNLHAYVGRALH 292  
QY 250 NAY-PSYISPTGCLPAHLGLGDMWGRFTNLYSLTVPGQKPNIDVTAMVDQANDQARIF 308  
DB 293 RHYGAQHINLEGPITPAHLGLGNWAQVNSIYDLVAPPPSASTMDATEAMIKOGTTPRMF 352  
QY 309 KEAEKFFVSVCPLPNMTQGWNSMLTDPGNVOKAVCHPTAWDLGKG--DFRILMCTKVTMD 367  
DB 353 EADKFFISLGLLPVPPEFWNKSMLKEPTDGRVNVCHASAWDFVNGDFRDKQTSVNE 412  
QY 368 DELTAHHEMGHIQYDMAYAAQFLLRNGANEGHEAVGEIMSLSAATPKHLKSLGLSPD 427  
DB 413 DLVVVHHEMGHIQYFMQYKDLPLVALREGANPGFHEAIGDVLALSVSPKHLHSLNLLSSE 472  
QY 428 FQEDNETEINFLKQALITVGLTPFTYMLEKRWMPKGEIPKQDWMKKWEMKREIVGV 487  
DB 473 -GGYEHDIINFLMKALDKIAFIPFSYLVDEWRVFDGSIITKENYQEWNSLRKYQGL 531  
QY 488 VEPVPHDETCDPASLPHVSNDSYRIVYRTRLYQFQFQALCOAAKHEGPHKCDLSNS 547  
DB 532 CPPAPRSQGDGDPGAKFHPSSVPYRIVYRISFIQFQFHEALCKAAGHTGPLTCDIYQS 591  
QY 548 TEAGOKLFNMLRGLKSEPTWLALENVVGAKNMNVRLLNYPFLTWLKDQNK--KNSFVG 605  
DB 592 KEAGKRLADAMKLGYSKQWPEAMKITGQPNMSASAIMVFKPLTEWLVTEVNRHGETL 651  
QY 606 W-STDWSPYADQS 617  
DB 652 WFOYTWTPNSARS 664





QY	128	STGKVCNPNPQC-	LLEPLGLNBIMANSLDYNERLMAWESWRSGKQLRPYLEEYVL	186
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	128	AKVKVCDYKDSTKDALDPAIEIEVISKSROHEELAYVRIFYDKAGTAVRSQFERYVEL	187	
QY	187	KMEMARANIYEDGYTWRGDYFYNGVDGYDYSRGQLTIEDVHTPEIKPLRYEHLHAYRA	246	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	188	NTKAAKLNNFTSGAEAWLDEYE-----DDTFQQLEDI---FADIRPLLPADFWLCAP	237	
QY	247	KLMNA-PSYISPIGCLPAHLIGDMWGREFWNLYSLTVPGQKNIDYTDAMVDCQAWDAQ	305	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	238	RURKHGYDAVVSSTGIPMHLNNMQAQNSEIADIYSPFEKPPLDVSAEMEKAQYTPL	297	
QY	306	RIFKEAKEFVSVGLPNMTQGFWNSMLTPDGNYQKAVCHPTAWDLGK-GOFRIILMCTKV	364	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	298	KMFQMGGDDFTSMNLTKLPQDFWDKSIEXPTDGRDLVCHASAMD FYLLIDDVRIKQTRV	357	
QY	365	TWDDFLTAIHENGHIQYDMAAQAOPFLLRNGANGFGHEAVGEIMSLSAATPKLXSIGLL	424	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	358	TODQLFTVHHELGHIOYFLOQYQHQPFFVRTGANPGFHEAVGDVLSVTSVPKHLEKIGLL	417	
QY	425	SPDFQEDNETENFLLKQALITVGLPTFMLEKRWNVKFCEIPTKDOMMKWEMEKREI	484	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	418	K-DYVRDDRGINQLFLTALDKITVFUPFATMTDIRWSLFSEYVDKANWCFAFKLRDEY	476	
QY	485	VGVWPVPVPHDETCDPASLFHVSNDSYFIYYTTLTQFOQEALC-QAAKH-----EGP	538	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	477	SGIEPPVVRSEXDFDAPAKYHISADVEYLRLYSFIYQFOYKACIACAGQVDPDNVELP	536	
QY	539	LHKCDISNSTEAGOKUFNNMLRLGKSEPWTALLENVVGAKNMNVRPLLNFYEPFLFTWKDQ	598	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	537	LONCDIYGSARAGAATHNMLSMSGASKPWPDALLEAFNGERTMSGRAIAEYFEFLRVWLAE	596	
QY	599	N--KNSFVGWST	608	
Db	:	:	:   :   :   :   :   :   :   :   :   :   :   :	
Db	597	NKKNNVHICWTT	608	

RESULT 12

RESULT 11  
A57533

peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (*Drosophila melanogaster*)  
N;Alternate names: angiotensin-converting enzyme  
C;Species: *Drosophila melanogaster*  
C;Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 26-Feb-1998  
C;Accession: A57533  
R;Comment: Williams, T.A.; Lanango, N.S.; Coates, D.; Corvol, P.; Soubrier, F.; H  
J. Biol. Chem. 270, 13613-13619, 1995  
A;Title: Cloning and expression of an evolutionary conserved single-domain angiotensin o  
A;Reference number: A57533; MUID:95293950

A;Accession: A57533  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-615 <COR>  
A;Cross-references: GB:U25344  
C;Genetics:  
C;Gene: FlyBase:Ance  
A;Cross-references: FlyBase:FBgn0012037  
C;Superfamily: mammalian peptidyl-dipeptidase A  
C;Keywords: peptidylpeptide hydrolase

Query Match	24.2%;	Score 1039;	DB 2;	Length 615;
Best Local Similarity	35.8%;	Pred. No. 7.2e-64;		
Matches 219;	Conservative 120;	Mismatches 251;	Indels 22;	Gaps 9;

8	LLSLVAVTAAQSTIEEQAKTFLDKFNHEADFLYQSSLASWNYNTNITEENVQNMNAGD	67
QY	:	
8	LLATLAVTQALVKEEIQKEYLENLKEAKRTNVETAAWAYGNSITDENKKKEISA	67
Db	:	
68	KWSAFLKREQSTLAQWPIQEIQLTVKLQALQALQSSVLSEDKSKRLNTILNTMSTIY	127
QY	:	
68	ELAFPMKEVASDPTTKFQWRNSYQSEDLKROFKALTKLGYAALPEDDYAELLDTLSAMESNF	127
Db	:	

Db 195 RLTRKASQLNGHRSYADYVYQFVE-----DPDFER-----QIDATFKQLLLPLYRLQLHGIV 244  
QY 245 RAKLMNAY--PSYISPIGCLPAHLGDMGWRFTWLYSLTVFPGQKPNIDVDVTDAMVDQAWD 303  
Db 245 RFLRQHYGPDVMPAEGNIPISLGNMGQSNELLDFTPYPEKFPVDVRAEMEKOQYT 304  
QY 304 AQRIKAEAEFFVSVGLPNNMTOGFWENSLTDPGNVOKAVCHPTAWDLGK-GDFRILMCT 362  
Db 305 VOKLFELGDOFOSLGRMRALPPSFNUSVLTTRPD-KQVVCASAWDFYQSDVRKIMCT 363  
QY 363 KYTMDDFLAHHEMGHIQYDMAYAAQFLLRNGANEGFHEAVGETMSLSAATPKHLKSTG 422  
Db 364 EVDSHYFVYVHGLGHIOYLYEQQPAVYRGANPGFHEAVGDVIALSVMSAKHLKAIG 423  
QY 423 LLSPOFQEDNETEINFLKQALITVGLPFTYMLEKRWMMVFKGIPKQDMKKWEMKR 482  
Db 424 LIE-NGRLDEKSRINQLFKQALSIVELPGYAYDVYKRYAVFERNELDESQWNCGEQWMS 482  
QY 483 EIVGVVEPHDETYCDPASLFHVSNDYSFIRYTRTLYQFOFQFQALCOAAKHEGP---- 538  
Db 483 EFGGVPEPVFTEKDEDPAPAKYHLDADVEYLRYFAAHIFQFQHKVLCRKAGQYAPNNSR 542  
QY 539 --LHKDCISNSTAGOKLFNMLRGKSEPTLALENVYGAKNMVRPLLNYEPLFTWLK 596  
Db 543 LITDNCIDFGSKAAGRSLSQFLSKGNSRHWKEVLEETGETEMDPAALLEYEPFLYQWLK 602  
QY 597 DQNKNSFVGWSTDWSP 612  
Db 603 QE--NSRLGVPLGWGP 616  
RESULT 13  
T15792  
hypothetical protein C42D8.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
R:Hallsworth, K.  
submitted to the EMBL Data Library, April 1996  
A:Description: The sequence of C. elegans cosmid C42D8.  
A:Reference number: Z18405  
A:Accession: T15792  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-907 <HAL>  
A:Cross-references: EMBL:U56966; NID:g1293844; PID:g1293847; PIDN:AAA98719.1; GSPDB:GNO0  
A:Experimental source: strain Bristol N2; clone C42D8  
C:Genetics:  
A:Gene: CESP:C42D8.5  
A:Map position: X  
A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3  
Query Match 15.08; Score 642.5; DB 2; Length 907;  
Best Local Similarity 27.08; Pred. No. 3.5e-36;  
Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps 19;  
QY 2 SSSSWLLSLVAVTAAOSTIEQAKTFDKFNHEAEDLFYQSSLASWNTNITEENVQN 61  
Db 160 SSNTWKTDNLQAPGSIKD--BEKURSLAGYEAEEAIKVLREVALSGWRYFNDAASPISLKA 217  
QY 62 MNAGDQWSAFLKQESTLAQMPQIEQNLTVKQLQALQOQNGSSVLSSEDKSRRLNTILN 121  
Db 218 LDEANVITMFVSTSMQAKOFDMASVTDEKVMRQLGYVFGMSALAPSRFADYSQAQA 277  
QY 122 TMSITYSTGKVCNPDNPQECILLLEPGLNEIMANSLDYNRLWAWESWRSEVGVKQLRPLYE 181  
Db 278 ALNRDSKDSITCDKDVPPCALQKIDMSIPRNXKDSRLQLHLWVYVTAIAKS-KPSYN 336  
QY 182 EYVVLKMEMARANHYEDYGTWRGDIYVNG-VGDYDYSRGLIEDVEHTEEFKPLYEHL 240  
Db 337 NIITISNEGAKLNGFANGGAMWRSAPDMSKVHKAEEF--DLNKQIDKIYSTIQPFYQLL 393  
QY 241 HAYVRKLMNAY--PSYISPIGCLPAHLGDMGWRFTWLYSLTVFPGQKPNIDVDVTDAMV 298

Db 394 HAYMRQLAGIYSNPVGLSKDGPPIPAHLFGSLDGGDSAHYEQTKPFEESS--ETPEAML 451  
QY 299 D-----QAWDAQRIKAEAEFFVSVGLPNNMTOGFWENSLTDPGNVOKAVCHP-TAWDL-G 352  
Db 452 SAFNTQNTYTKMFVTAYRYKFSAGPHLPKSYTSTFARVWS-KDMICHPPAALDMRA 510  
QY 353 KGDFRILMCTKTVMDDFLTAHHEMGHIQYDMAYAAQFLLRNGANEGFHEAVGEIMSLSA 412  
Db 511 PNDFRVACAQGEPPFEQAHSLLVQTYOYLKDSLSLFEQASPVITDAIANAFHLS 570  
QY 413 ATPRHLKSIGLLSPDFQEDNETE-INFLKQALITVGLPFTYMLEKRWMMVFKGEIPKD 471  
Db 571 TNPHVLSQKLVSPSEHLDIKDSVIINKLYKESLESFTKLPFTTAADNWRVELFDCVTVPKN 630  
QY 472 QMMKKWEMKREIVGVVPEVPHDETYCDPASLFH--VSDYSFIRYTRIL-----YQFQF 525  
Db 631 KLNDRWWEIRNKYEGVRSPPQYNTSNLD--ALIHNSVSQVHS---PATRTLISYVLKFOI 685  
QY 526 QEALCOAA--KHEGPLHKCDISNSTEAGOKLFNMLRGKSEPTLALENVYGAKNMVR 582  
Db 686 LKALCQRELFWLSEG---CILSEDTF--EKLRETKLSSITWLKALEMISGKELDAQ 739  
QY 583 PLLNVFEPLFTWLKQDNK--NSFVGWSTDWSPYADQSI 618  
Db 740 PLLEYEFLINWLRNFTNEIDQVVGWDGEGTPTVEEI 777  
RESULT 14  
C83696  
hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, F.; H  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: C83696  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-532 <STO>  
A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04090.1; GSPDB:G  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH0371  
Query Match 3.7%; Score 157; DB 2; Length 532;  
Best Local Similarity 21.1%; Pred. No. 0.0058;  
Matches 118; Conservative 83; Mismatches 213; Indels 144; Gaps 29;  
QY 22 EEOAKTFDKFNHEAEDLFYQSSLASWNTNITEENVQNMMNAGDKWSAFLKQDS--- 77  
Db 3 EODIERFUSEQKRVEDLQVPLLNHMWVATTGEOESDKHEQSLSEYWAHFSDRFSQK 62  
QY 78 -----TLAQMYPLOEQNLTVKQLQALQOQNGSSVLSSEDKSRRLNTILNTMSTIY 127  
Db 63 VTRFRKIDSLPLMRQLDLDLHDKMIKNQFE--EGTRQOILSLE--KKISHVFTTFOPOV 118  
QY 128 STGKVCNPDNPQECILLLEPGLNEIMANSLDYNRLWAWESWRSEVGVKQLRPLYEYVVLK 187  
Db 119 NGSVRNSNNE-----LLDILRYDLDRERKQAWFA-SKEVGKTEKDLQLLRKR 166  
QY 188 NEMARANHYEDYGTWRGDIYVNGVDGYDSRGQIIEDEHT---FEETKPLYEHLHAVY 244  
Db 167 NEVARNLGFEFTF-----YHMSFATQELDEPQTFAMFETIKKSSDOAFMI 211  
QY 245 -----RAKLMNAYPSYISPIGCLPAHLGDMGWRFTWLYSLTVFPGQK-PNIDVDTA 296  
Db 212 KDEIDERAQVLKIKKDDLRLP-----WDYVDFPFQEAPESTIEHVD- 250  
QY 297 MYDQAWDAQRIKAEAEFFVSVGLPNNMTOGFWENSLTDPGNVOK-AVCHPTAWDLGKGD 355





